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## SEQUENCE LISTING

<110> Wei, Xin Gariepy , Jean

<120> LIBRARY OF TOXIN MUTANTS, AND METHODS OF USING SAME

<130> 34104-0082

<160> 7

<170> PatentIn version 3.2

<210> 1

<211> 299
<212> PRT
<213> Escherichia coli

<220>

<221> misc\_feature <223> Wild type SLT-1 A chain

<400> 1

Ile Glu Gly Arg Ala Ser Lys Glu Phe Thr Leu Asp Phe Ser Thr Ala 10

Lys Thr Tyr Val Asp Ser Leu Asn Val Ile Arg Ser Ala Ile Gly Thr 25 20

Pro Leu Glm Thr Ile Ser Ser Gly Gly Thr Ser Leu Leu Mat Ile Asp 35

Ser Gly Ser Gly Asp Asn Leu Phe Ala Val Asp Val Arg Gly Ile Asp 50

pro Glu Glu Gly Arg Phe Asn Asn Leu Arg Leu Ile Val Glu Arg Asn 75

Asn Leu Tyr Val Thr Gly Phe Val Asn Arg Thr Asn Asn Val Phe Tyr 'RS 90

Arg Phe Ala Asp Phe Ser His Val Thr Phe Pro Gly Thr Thr Ala Val . 110 100 105

Thr Leu Ser Gly Asp Ser Ser Tyr Thr Thr Leu Gln Arg Val Ala Gly 120

Ile Ser Arg Thr Gly Met Gln Ile Asn Arg His Ser Leu Thr Thr Ser

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Tyr Leu Asp Leu Met Ser His Ser Gly Thr Ser Leu Thr Gln Ser Val 150

Ala Arg Ala Met Leu Arg Phe Val Thr Val Thr Ala Glu Ala Leu Arg 170

Phe Arg Gln Ile Gln Arg Gly Phe Arg Thr Thr Leu Asp Asp Leu Ser 185

Gly Arg Ser Tyr Val Met Thr Ala Glu Asp Val Asp Leu Thr Leu Asn 200

Trp Gly Arg Leu Ser Ser Val. Leu Pro Asp Tyr His Gly Oln Asp Ser

Val Arg Val Gly Arg Ile Ser Phe Gly Ser Ile Asn Ala Ile Leu Gly 230

Ser Val Ala Leu Ile Leu Asn Cys His His His Ala Ser Arg Val Ala

Arg Met Ala Ser Asp Glu Phe Pro Ser Met Cys Pro Ala Asp Gly Arg

Val Arg Gly Ile Thr His Asn Lys Ile Leu Trp Asp Ser Ser Thr Leu 280 275

Gly Ala Ile Leu Met Arg Arg Thr Ile Ser Ser 295 290

<210> 2 <211> 32 <212> DNA

<213> Artificial

<220>

<223> Primer

<400> 2

gttactgtga cagctgaagc tttacgtttt cg

<210> 3 <211> 3 31

<212> DNA

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<223> Primer

32

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<400> 3 gagaagaaga gactgcagat tccatctgtt g

31

<210>

<211> 302

<212> PRT <213> Artificial

<223> SLT-1 A Chain lib#3 protein sequence (SAM3)

<400> 4

Lys Gly Met Arg Ser His His His His His His His Ile Glu Gly

Arg Ala Ser Lys Glu Phe Thr Leu Asp Phe Ser Thr Ala Lys Thr Tyr

Val Asp Ser Leu Asn Val Ile Arg Ser Ala Ile Gly Thr Fro Leu Gln 35

Thr Ile Ser Ser Gly Gly Thr Ser Leu Leu Met Ile Asp Ser Gly Ser

Gly Asp Asn Leu Phe Ala Val Asp Val Arg Gly Ile Asp Fro Glu Glu 70

Gly Arg Phe Asn Asn Leu Arg Leu Ile Val Glu Arg Asn Asn Leu Tyr

Val Thr Gly Phe Val Asn Arg Thr Asn Asn Val Phe Tyr Prg Phe Ala

Asp Phe Ser His Val Thr Phe Pro Gly Thr Thr Ala Val Thr Leu Ser

Gly Asp Ser Ser Tyr Thr Thr Leu Gln Arg Val Ala Gly Ile Ser Arg 140

Thr Gly Met Gln Ile Asn Arg His Ser Leu Thr Thr Ser Tyr Leu Asp 145

Leu Met Ser His Ser Gly Thr Ser Leu Thr Gln Ser Val Ala Arg Ala

Met Leu Arg Phe Val Thr Val Thr Ala Glu Ala Leu Arg Fhe Arg Gln

1.90

185 180

Ile Gln Arg Gly Phe Arg Thr Thr Leu Asp Asp Leu Ser Gly Arg Ser 200 205 195

Tyr Val Met Thr Ala Glu Asp Val Asp Leu Thr Leu Asn Trp Gly Arg 210 215

Leu Ser Ser Val Leu Pro Asp Tyr His Gly Gln Asp Ser Val Arg Val 225

Gly Arg Ile Ser Phe Gly Ser Ile Asn Ala Ile Leu Gly Ser Val Ala

Leu Ile Leu Asn Cys His His His Ile Tyr Ser Asn Lys Leu Met Ala

Ser Arg Val Ala Arg Met Ala Ser Asp Glu Phe Pro Ser Net Cys Pro

Ala Asp Gly Arg Val Arg Gly Ile Thr His Asn Lys Ile Leu 300 295

<210> 5

<211> 319

<212> PRT <213> Artificial

<223> SLT-1 A Chain lib#5 protein sequence (SAM5)

**<400>** 5

Lys Gly Met Arg Ser His His His His His His His Ile Glu Gly

Arg Ala Ser Lys Glu Phe Thr Leu Asp Phe Ser Thr Ala Lys Thr Tyr

Val Asp Ser Leu Asn Val Ile Arg Ser Ala Ile Gly Thr Fro Leu Gln 40 35

Thr Ile Ser Ser Gly Gly Thr Ser Leu Leu Met Ile Asp Ser Gly Ser 50

Gly Asp Asn Leu Phe Ala Val Asp Val Arg Gly Ile Asp Fro Glu Glu

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Gly Arg Phe Asn Asn Leu Arg Leu Ile Val Glu Arg Asn Asn Leu Tyr 85 90 95

Val Thr Gly Phe Val Asn Arg Thr Asn Asn Val Phe Tyr Arg Phe Ala

Asp Phe Ser His Val Thr Phe Pro Gly Thr Thr Ala Val Thr Leu Ser 115 120 125

Gly Asp Ser Ser Tyr Thr Thr Leu Gln Arg Val Ala Gly lle Ser Arg 130 140

Thr Gly Met Gln Ile Asn Arg His Ser Leu Thr Thr Ser Tyr Leu Asp 145 150 155

Leu Met Ser His Ser Gly Thr Ser Leu Thr Gln Ser Val 1.1a Arg Ala 165 170 175

Met Leu Arg Phe Val Thr Val Thr Ala Glu Ala Leu Arg Fhe Arg Cln 180 185 190

Ile Gin Arg Gly Phe Arg Thr Thr Leu Asp Asp Leu Ser Cly Arg Ser 195 200 205

Tyr Val Met Thr Ala Glu Asp Val Asp Leu Thr Leu Asn Trp Gly Arg 210 220

Leu Ser Ser Val Leu Pro Asp Tyr His Gly Gln Asp Ser Val Arg Val 225 230 235 240

Gly Arg Ile Ser Phe Gly Ser Ile Asn Ala İle Leu Gly Ser Val Ala 245 250 255

Leu Ile Leu Asn Cys His His His Ala Ala Phe Ala Asp Ieu Ile Ala 260 265 270

Ser Arg Val Ala Arg Met Ala Ser Asp Glu Phe Pro Ser Met Cys Pro 275 280 285

Ala Asp Gly Arg Val Arg Gly Ile Thr His Asn Lys Ile Leu Trp Asp 290 295 300

Ser Ser Thr Leu Gly Ala Ile Leu Met Arg Arg Thr Ile Ser Ser 305 315

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